



FIG. 1A

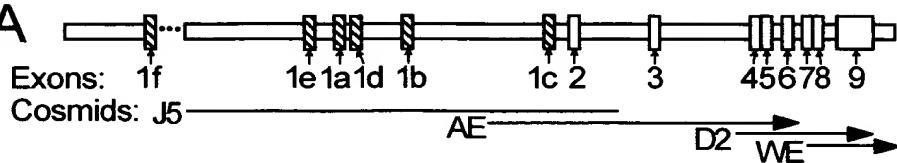
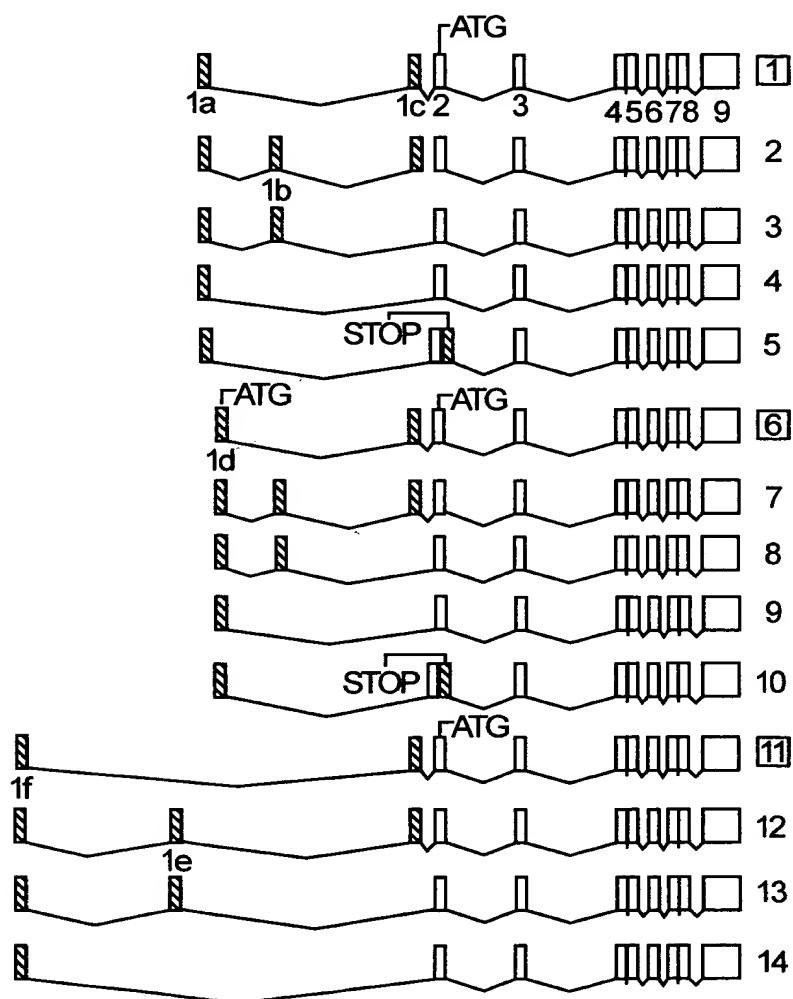


FIG. 1B



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FIG. 1C

(SEQ ID NO.14)

Transcript 1:
Transcript 6: MEWRNKKRSDWLSMVLRTAGVEEAFGSEVSVRPHR
RAPLGSYLPMEAMA
Transcript 9:
MEW RNKKR SDWL SMMRLTAGVEG MEAMA

MEAMA ASTSLPDPGD FDRNV PRI DBD 427aa ←
MEAMA ASTSLPDPGD FDRNV PRI DBD 477aa ←
MEW RNKKR SDWL SMMRLTAGVEG MEAMA ASTSLPDPGD FDRNV PRI DBD 450aa ←

(SEQ ID NO.16)

(SEQ ID NO.15)

FIG. 4

- A. 5'...atcccttaag GGCTCCTGAACCTAGCCCCAGCTGGACGGAG
AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCCC
CGTGACATTGCTTGCCTCCCTCAATCCTCATAGCT
TCTCTTGGGgttaagtacag...3' (SEQ ID NO: 13)

- B. 5'...TGCGACCTTGGCGGTGAGCCTGGGGACAGGGGTGAGGC
CAGAGACGGACGGACGCAGGGGCCCCGGCOCAGGGGGAGGG
AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGGGGTGTG
TTCACCCGCAGCCCAATCCATCACTCAGCAACTCCTAGAC
GCTGGTAGAAAGTTCTCGAGGGAGCCTGCCATCCAGTCGT
GCGTGCAG...3' (SEQ ID NO: 5)

- C. 5'...tgtttttag AGGCAGCATGAAACAGTGGATGTGCAGAG
AGAAGATCTGGGTCCAGTAGCTCTGACACTCTCAGCTGT
AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA
CGGTATTTTACTCTCATGTCTGAAAAGGCTATGATAA
AGATCAAgttaagatatt...3' (SEQ ID NO: 6)

- D. 5'...GTTTCTTCTTCTGTCGGGGCGCCTTGGC ATGGAGTG
AGGAATAAGAAAAGGAGCGATTGGCTGTCGATGGGTGCTCA
GAACTGCTGGAGTGGAGGgtgttaacc...3' (SEQ ID NO: 1)

FIG. 5A

Transcript 6

(Sequence Range: 1 to 1463)

10 20 30 40 50
* * * * * * * * *
GTTTCCTCTCT TCTGTGGGG CGCCTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
MetGluTrpArg AsnLysLys>

60 70 80 90 100
* * * * * * * * *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGAAGC
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCTTCG
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGluAla>

110 120 130 140 150
* * * * * * * * *
CTTTGGGTCT GAAAGTGTCTG TGAGACCTCA CAGAAGAGCA CCCCTGGGCT
GAAACCCAGA CTTCACAGAC ACTCTGGAGT GTCTTCTCGT GGGGACCCGA
PheGlySer GluValSer ValArgProHis ArgArgAla ProLeuGly>

160 170 180 190 200
* * * * * * * * *
CCACTTACCT GCCCCCTGCT CCTTCAGGGTA TGGAGGAAT GGCAGGCCAGC
GGTGAATGGA CGGGGGACGA GGAAGTCCCT ACCTCCGTTA CCGCCGGTCG
SerThrTyrLeu ProProAla ProSerGly MetGluAlaMet AlaAlaSer>

210 220 230 240 250
* * * * * * * * *
ACTTCCCTGC CTGACCTCTGG AGACTTTGAC CGGAACGTGC CCCGGATCTG
TGAAGGGACG GACTGGGACC TCTGAAACTG GCCTTGCACG GGGCCTAGAC
ThrSerLeu ProAspProGly AspPheAsp ArgAsnVal ProArgIleCys>

260 270 280 290 300
* * * * * * * * *
TGGGGTGTGT GGAGACCGAG CCACTGGCTT TCACCTCAAT GCTATGACCT
ACCCCCACACA CCTCTGGCTC GGTGACCGAA AGTGAAGTTA CGATACTGGA
GlyValCys GlyAspArg AlaThrGlyPhe HisPheAsn AlaMetThr>

310 320 330 340 350
* * * * * * * * *
GTGAAGGCTG CAAAGGCTTC TTCAAGGCAGA GCATGAAGCG GAAGGCACCA
CACTTCCGAC GTTTCCGAAG AAGTCCGCTT CGTACTTCGC CTTCCGTGAT
CysGluGlyCys LysGlyPhe PheArgArg SerMetLysArg LysAlaLeu>

360 370 380 390 400
* * * * * * * * *
TTTACCTGCC CCTTCAACGG GGACTGCCGC ATCACCAAGG ACAACCGACG
AAGTGGACGG GGAAGTTGCC CCTGACGGCG TAGTGGTTCC TGTTGGCTGC
PheThrCys ProPheAsnGly AspCysArg IleThrLys AspAsnArgArg>

FIG. 5B

410 420 430 440 450
* * * * *
CCACTGCCAG GCCTGCCGGC TCAAACGCTG TGTGGACATC GGCATGATGA
GGTGACGGTC CGGACGGCCG AGTTGCGAC ACACCTGTAG CCGTACTACT
HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet>

460 470 480 490 500
* * * * *
AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC
TCCTCAAGTA AGACTGTCTA CTCTTCACG TCTCCTTCGC CCTCTACTAG
LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle>

510 520 530 540 550
* * * * *
CTGAAGCGGA AGGAGGAGGA GGCTTGAAG GACAGTCTGC GCCCCAAGCT
GACTTCGCCT TCCTCCTCCT CCGGAACCTTC CTGTCAGACG CCGGGTTCGA
LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu>

560 570 580 590 600
* * * * *
GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACATA
CAGACTCCTC GTCGTCGGT AGAACGGTA TGACGACCTG CGGGTGGTAT
SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis>

610 620 630 640 650
* * * * *
AGACCTACGA CCCCACCTAC TCCGACTTCT GCCAGTTCCG GCCTCCAGTT
TCTGGATGCT GGGGTGGATG AGGCTGAAGA CGGTCAAGGC CGGAGGTCAA
LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal>

660 670 680 690 700
* * * * *
CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCA ACTCCAGACA
GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT
ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis>

710 720 730 740 750
* * * * *
CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCCTGCTCA GATCACTGTA
GTGAGGGTCG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT
ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys>

760 770 780 790 800
* * * * *
TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG
AGTGGAGAAG TCTGTACTAC CTGAGCAGGT CGAAGAGGTT AGACCTAGAC
IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu>

810 820 830 840 850
* * * * *
AGTGAAGAAG ATTCAAGATGA CCCTCTGTG ACCCTAGAGC TGTCCAGCT
TCACTCTTC TAAGTCTACT GGGAAAGACAC TGGGATCTG ACAGGGTCGA
SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>

FIG. 5C

860 870 880 890 900
* * * * *
CTCCATGCTG CCCCACCTGG CTGACCTGGT CAGTTACAGC ATCCAAAAGG
GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTGC TAGGTTTCC
SerMetLeu ProHisLeu AlaAspLeuVal SerTyrSer IleGlnLys>

910 920 930 940 950
* * * * *
TCATTGGCTT TGCTAACGATG ATACCAGGAT TCAGAGACCT CACCTCTGAG
AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA GTGGAGACTC
ValIleGlyPhe AlaLysMet IleProGly PheArgAspLeu ThrSerGlu>

960 970 980 990 1000
* * * * *
GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTCA TCATGTTGCG
CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAGT AGTACAACGC
AspGlnIle ValLeuLeuLys SerSerAla IleGluVal IleMetLeuArg>

1010 1020 1030 1040 1050
* * * * *
CTCCAATGAG TCCTTCACCA TGGACGACAT GTCCTGGACC TGTGGCAACC
GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCTGG ACACCCTGG
SerAsnGlu SerPheThr MetAspAspMet SerTrpThr CysGlyAsn>

1060 1070 1080 1090 1100
* * * * *
AAGACTACAA GTACCGCGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG
TTCTGATGTT CATGGCGCAG TCACTGCCTG TTGTTCTGGCC TGTGTCGGAC
GlnAspTyrLys TyrArgVal SerAspVal ThrLysAlaGly HisSerLeu>

1110 1120 1130 1140 1150
* * * * *
GAGCTGATTG AGCCCCTCAT CAAGTTCCAG GTGGGACTGA AGAACGCTGAA
CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCCCTGACT TCTTCGACTT
GluLeuIle GluProLeuIle LysPheGln ValGlyLeu LysLysLeuAsn>

1160 1170 1180 1190 1200
* * * * *
CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC
GAACGTACTC CTCCTCGTAC AGGACCGAGTA CCGGTAGACG TAGCAGAGGG
LeuHisGlu GluGluHis ValLeuLeuMet AlaIleCys IleValSer>

1210 1220 1230 1240 1250
* * * * *
CAGATCGTCC TGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC
GTCTAGCAGG ACCCCACGTC CTGCGCGCG ACTAACTCCG GTAGGTCTTG
ProAspArgPro GlyValGln AspAlaAla LeuIleGluAla IleGlnAsp>

1260 1270 1280 1290 1300
* * * * *
CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCCC
GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGCGGGGG
ArgLeuSer AsnThrLeuGln ThrTyrIle ArgCysArg HisProProPro>

FIG. 5D

1310 1320 1330 1340 1350
* * * * * * * * * * * * * * * * * * * *
GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC
CCCGTCGGTG GACGAGATAc GGTTCTACTA GGTCTTCGAT CGGCTGGACG
GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu>

1360 1370 1380 1390 1400
* * * * * * * * * * * * * * * * * * * *
GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCCTCCAG
CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGCGGACGGA GAGGAAGGTC
ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln>

1410 1420 1430 1440 1450
* * * * * * * * * * * * * * * * * * * *
CCTGAGTGCA GCATGAAGCT AACGCCCTT GTGCTCGAAC TGTTTGGCAA
GGACTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAAACCGTT
ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn>

1460
* *
TGAGATCTCC TGA (SEQ ID NO:2)
ACTCTAGAGG ACT (SEQ ID NO:17)
GluIleSer ***>(SEQ ID NO:9)



FIG. 6A

Transcript 9
(Sequence range: 1 to 1382)

10 20 30 40 50
* * * * * * * * *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
MetGluTrpArg AsnLysLys>

60 70 80 90 100
* * * * * * * * *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

110 120 130 140 150
* * * * * * * * *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

160 170 180 190 200
* * * * * * * * *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

210 220 230 240 250
* * * * * * * * *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGCGAAG
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCGAAGA AGTCCGCTTC
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArgArgSer>

260 270 280 290 300
* * * * * * * * *
CATGAAGCGG AAGGCACTAT TCACCTGCC CTTCAACGGG GACTGCCGCA
GTACTTCGCC TTCCGTGATA AGTGGACGGG GAAGTTGCC CTGACGGCGT
MetLysArg LysAlaLeu PheThrCysPro PheAsnGly AspCysArg>

310 320 330 340 350
* * * * * * * * *
TCACCAAGGA CAACCGACGC CACTGCCAGG CCTGCCGGCT CAAACGCTGT
AGTGGTTCCCT GTTGGCTGCG GTGACGGTCC GGACGGCCGA GTTGCGACA
IleThrLysAsp AsnArgArg HisCysGln AlaCysArgLeu LysArgCys>

360 370 380 390 400
* * * * * * * * *
GTGGACATCG GCATGATGAA GGAGTTCATT CTGACAGATG AGGAAGTGCA
CACCTGTAGC CGTACTACTT CCTCAAGTAA GACTGTCTAC TCCTTCACGT
ValAspIle GlyMetMetLys GluPheIle LeuThrAsp GluGluValGln>

FIG. 6B

410 420 430 440 450
* * * * *
GAGGAAGCGG GAGATGATCC TGAAGCGGAA GGAGGAGGGAG GCCTTGAAGG
CTCCTTCGCC CTCTACTAGG ACTTCGCCTT CCTCCTCCTC CGGAACATTCC
ArgLysArg GluMetIle LeuLysArgLys GluGluGlu AlaLeuLys>

460 470 480 490 500
* * * * *
ACAGTCTGCG GCCCAAGCTG TCTGAGGAGC AGCAGCGCAT CATTGCCATA
TGTCAGACGC CGGGTTGAC AGACTCCTCG TCGTCCGCTA GTAACGGTAT
AspSerLeuArg ProLysLeu SerGluGlu GlnGlnArgIle IleAlaIle>

510 520 530 540 550
* * * * *
CTGCTGGACG CCCACCATAA GACCTACGAC CCCACCTACT CCGACTTCTG
GACGACCTGC GGGTGGTATT CTGGATGCTG GGGTGGATGA GGCTGAAGAC
LeuLeuAsp AlaHisHisLys ThrTyrAsp ProThrTyr SerAspPheCys>

560 570 580 590 600
* * * * *
CCAGTTCCGG CCTCCAGTTC GTGTGAATGA TGGTGGAGGG AGCCATCCTT
GGTCAAGGCC GGAGGTCAAG CACACTTACT ACCACCTCCC TCGGTAGGAA
GlnPheArg ProProVal ArgValAsnAsp GlyGlyGly SerHisPro>

610 620 630 640 650
* * * * *
CCAGGCCCAA CTCCAGACAC ACTCCCAGCT TCTCTGGGA CTCCTCCTCC
GGTCCGGGTT GAGGTCTGTG TGAGGGTCGA AGAGACCCCT GAGGAGGAGG
SerArgProAsn SerArgHis ThrProSer PheSerGlyAsp SerSerSer>

660 670 680 690 700
* * * * *
TCCTGCTCAG ATCACTGTAT CACCTCTTCA GACATGATGG ACTCGTCCAG
AGGACGAGTC TAGTGACATA GTGGAGAAGT CTGTACTACC TGAGCAGGTC
SerCysSer AspHisCysIle ThrSerSer AspMetMet AspSerSerSer>

710 720 730 740 750
* * * * *
CTTCTCCAAT CTGGATCTGA GTGAAGAAGA TTCAGATGAC CCTTCTGTGA
GAAGAGGTTA GACCTAGACT CACTTCTCT AAGTCTACTG GGAAGACACT
PheSerAsn LeuAspLeu SerGluGluAsp SerAspAsp ProSerVal>

760 770 780 790 800
* * * * *
CCCTAGAGCT GTCCCAGCTC TCCATGCTGC CCCACCTGGC TGACCTGGTC
GGGATCTCGA CAGGGTCCAG AGGTACGACG GGGTGGACCG ACTGGACCAAG
ThrLeuGluLeu SerGlnLeu SerMetLeu ProHisLeuAla AspLeuVal>

810 820 830 840 850
* * * * *
AGTTACAGCA TCCAAAAGGT CATTGGCTTT GCTAAGATGA TACCAAGGATT
TCAATGTCGT AGGTTTCCA GTAACCGAAA CGATTCTACT ATGGTCCTAA
SerTyrSer IleGlnLysVal IleGlyPhe AlaLysMet IleProGlyPhe>

FIG. 6C

860 870 880 890 900
* * * * *
CAGAGACCTC ACCTCTGAGG ACCAGATCGT ACTGCTGAAG TCAAGTGCCA
GTCTCTGGAG TGGAGACTCC TGTTCTAGCA TGACGACTTC AGTTCACGGT
ArgAspLeu ThrSerGlu AspGlnIleVal LeuLeuLys SerSerAla>
910 920 930 940 950
* * * * *
TTGAGGTCAT CATGTGCGC TCCAATGAGT CCTTCACCAT GGACGACATG
AACTCCAGTA GTACAACGCG AGGTTACTCA GGAAGTGGTA CCTGCTGTAC
IleGluValIle MetLeuArg SerAsnGlu SerPheThrMet AspAspMet>
960 970 980 990 1000
* * * * *
TCCTGGACCT GTGGCAACCA AGACTACAAG TACCGCGTCA GTGACGTGAC
AGGACCTGGA CACCGTTGGT TCTGATGTTC ATGGCGCAGT CACTGCACTG
SerTrpThr CysGlyAsnGln AspTyrLys TyrArgVal SerAspValThr>
1010 1020 1030 1040 1050
* * * * *
CAAAGCCGGA CACAGCCTGG AGCTGATTGA GCCCCTCATC AAGTTCCAGG
GTTTCGGCCT GTGTCGGACC TCGACTAAT CGGGGAGTAG TTCAAGGTCC
LysAlaGly HisSerLeu GluLeuIleGlu ProLeuIle LysPheGln>
1060 1070 1080 1090 1100
* * * * *
TGGGACTGAA GAAGCTGAAC TTGCATGAGG AGGAGCATGT CCTGCTCATG
ACCTGACTT CTTCGACTTG AACGTACTCC TCCTCGTACA GGACGAGTAC
ValGlyLeuLys LysLeuAsn LeuHisGlu GluGluHisVal LeuLeuMet>
1110 1120 1130 1140 1150
* * * * *
GCCATCTGCA TCGTCTCCCC AGATCGCTT GGGGTGCAGG ACGCCGCGCT
CGGTAGACGT AGCAGAGGGG TCTAGCAGGA CCCCACGTCC TGCAGCGCGA
AlaIleCys IleValSerPro AspArgPro GlyValGln AspAlaAlaLeu>
1160 1170 1180 1190 1200
* * * * *
GATTGAGGCC ATCCAGGACC GCCTGTCCAA CACACTGCAG ACGTACATCC
CTAACTCCGG TAGGTCTGG CGGACAGGTT GTGTGACGTC TGCATGTAGG
IleGluAla IleGlnAsp ArgLeuSerAsn ThrLeuGln ThrTyrIle>
1210 1220 1230 1240 1250
* * * * *
GCTGCCGCCA CCCGCCCCCG GGCAGCCACC TGCTCTATGC CAAGATGATC
CGACGGCGGT GGGCGGGGGC CCGTCGGTGG ACGAGATAACG GTTCTACTAG
ArgCysArgHis ProProPro GlySerHis LeuLeuTyrAla LysMetIle>
1260 1270 1280 1290 1300
* * * * *
CAGAAGCTAG CCGACCTGCG CAGCCTCAAT GAGGAGCACT CCAAGCAGTA
GTCTTCGATC GGCTGGACGC GTCGGAGTTA CTCCTCGTGA GGTTCGTCAT
GlnLysLeu AlaAspLeuArg SerLeuAsn GluGluHis SerLysGlnTyr>

FIG. 6D

1310 1320 1330 1340 1350
* * * * * * * * * * * * * * * * * * * *
CCGCTGCCTC TCCTTCCAGC CTGAGTCAG CATGAAGCTA ACGCCCCCTTG
GGCGACGGAG AGGAAGGTG GACTCACGTC GTACTTCGAT TGCGGGGAAC
ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>

1360 1370 1380
* * * * * * * * * * * * * * *
TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA (SEQ ID NO:3)
ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT (SEQ ID NO:18)
ValLeuGluVal PheGlyAsn GluIleSer ***> (SEQ ID NO:10)

FIG. 7A

Transcript 10 (Sequence Range: 1 to 1534)

10 20 30 40 50
*
GTTTCCTCTCT TCTGTCGGGG CGCCTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
MetGluTrpArg AsnLysLys>

60 70 80 90 100
*
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

110 120 130 140 150
*
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

160 170 180 190 200
*
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGACCGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

210 220 230 240 250
*
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGTGAGC
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCACTCG
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArg*** (SEQ ID NO:11)

260 270 280 290 300
*
CCCCCTCCCCA GGCTCTCCCC AGTGGAAAGG GAGGGAGAAG AAGCAAGGTG
GGGGGAGGGT CCGAGAGGGG TCACCTTCC CTCCCTCTTC TTCGTTCCAC

310 320 330 340 350
*
TTTCCATGAA GGGAGCCCTT GCATTTTCA CATCTCCTTC CTTACAATGT
AAAGGTACTT CCCTCGGGAA CGTAAAAAGT GTAGAGGAAG GAATGTTACA

360 370 380 390 400
*
CCATGGAAACA TGCAGCGCTC ACAGGCCACAG GAGCAGGAGG GTCTTGGCGA
GGTACCTTGT ACGCCGCGAG TGTGGTGTC CTCGTCTCC CAGAACCGCT

FIG. 7B

410 420 430 440 450
* * * * *
AGCATGAAGC GGAAGGCACT ATTCACCTGC CCCTTCAACG GGGACTGCCG
TCGTACTTCG CCTTCCGTGA TAAGTGGACG GGGAAAGTTGC CCCTGACGGC

460 470 480 490 500
* * * * *
CATCACCAAG GACAACCGAC GCCACTGCCA GGCCCTGCCGG CTCAAACGCT
GTAGTGGTTC CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCAG

510 520 530 540 550
* * * * *
GTGTGGACAT CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG
CACACCTGTA GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC

560 570 580 590 600
* * * * *
CAGAGGAAGC GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA
GTCTCCTTCG CCCTCTACTA GGACTTCGCC TTCCCTCCTCC TCCGGAACCTT

610 620 630 640 650
* * * * *
GGACAGTCTG CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA
CCTGTCAGAC GCCGGGTTCG ACAGACTCCT CGTCGTGCGG TAGAACGGT

660 670 680 690 700
* * * * *
TACTGCTGGA CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC
ATGACGACCT GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG

710 720 730 740 750
* * * * *
TGCCAGTTCC GGCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC
ACGGTCAAGG CGGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG

760 770 780 790 800
* * * * *
TTCCAGGCC AACTCCAGAC ACACCTCCAG CTTCTCTGGG GACTCCTCCT
AAGGTCCGGG TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA

810 820 830 840 850
* * * * *
CCTCCTGCTC AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC
GGAGGACGAG TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG

860 870 880 890 900
* * * * *
AGCTTCTCCA ATCTGGATCT GAGTGAAGAA GATTCAAGATG ACCCTTCTGT
TCGAAGAGGT TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA

910 920 930 940 950
* * * * *
GACCCTAGAG CTGTCCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG
CTGGGATCTC GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC

FIG. 7C

960 970 980 990 1000
TCAGTTACAG CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA
AGTCAATGTC GTAGGTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT
1010 1020 1030 1040 1050
TTCAGAGACC TCACCTCTGA GGACCGAGTC GTACTGCTGA AGTCAAGTGC
AAGTCTCTGG AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG
1060 1070 1080 1090 1100
CATTGAGGTC ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA
GTAACCTCCAG TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT
1110 1120 1130 1140 1150
TGTCCCTGGAC CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG
ACAGGACCTG GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC
1160 1170 1180 1190 1200
ACCAAAGCCG GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA
TGGTTTCGGC CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT
1210 1220 1230 1240 1250
GGTGGGACTG AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA
CCACCCCTGAC TTCCTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT
1260 1270 1280 1290 1300
TGGCCATCTG CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG
ACCGGTAGAC GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC
1310 1320 1330 1340 1350
CTGATTGAGG CCATCCAGGA CCCCTGTCC AACACACTGC AGACGTACAT
GACTAACTCC GGTAGGTCCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA
1360 1370 1380 1390 1400
CCGCTGCCGC CACCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA
GGCGACGGCG GTGGGCGGGG GCCCCGCGGT GGACGAGATA CGGTTCTACT
1410 1420 1430 1440 1450
TCCAGAACGCT AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG
AGGTCTTCGA TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC
1460 1470 1480 1490 1500
TACCGCTGCC TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCCT
ATGGCGACGG AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA

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OCT 22 2002
PATENT & TRADEMARK OFFICE
Title: "Isoforms of the Human Vitamin D Receptor"
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Atty. Docket No. RICE-014

FIG. 7D

1510 1520 1530
* * * *
TGTGCTCGAA GTGTTGGCA ATGAGATCTC CTGA (SEQ ID NO:4)
ACACGAGCTT CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:19)

FIG. 8A

10 *
 20 *
 30 *
 40 *
 50 *
 TCGGACCTTG GCGGTGAGCC TGGGGACAGG GGTGAGGCCA GAGACGGACG
 ACGCTGGAAC CGCCACTCGG ACCCTGTCC CCACTCCGGT CTCTGCCTGC
 60 *
 70 *
 80 *
 90 *
 100 *
 GACGCAGGGG CCCGGCCCAA GGCAGGGAG AACAGGGCA CTAAGGCAGA
 CTGCGTCCCC GGGCGGGTT CCGCTCCCTC TTGTCGCCGT GATTCCGTCT
 110 *
 120 *
 130 *
 140 *
 150 *
 AAGGAAGAGG GCGGTGTGTT CACCCGCAGC CCAATCCATC ACTCAGCAAC
 TTCCTCTCC CGCCACACAA GTGGCGTGT GGTTAGGTAG TGAGTCGTTG
 160 *
 170 *
 180 *
 190 *
 200 *
 TCCTAGACGC TGGTAGAAAG TTCCTCCAG GAGCCTGCCA TCCAGTCGTG
 AGGATCTGCG ACCATCTTC AAGGAGGCTC CTCGGACGGT AGGTCAAGCAC
 210 *
 220 *
 230 *
 240 *
 250 *
 CGTGCAGAAC CCTTTGGGTC TGAAGTGTCT GTGAGACCTC ACAGAAGAGC
 GCACGTCTTC GGAAACCCAG ACTTCACAGA CACTCTGGAG TGTCTCTCG
 260 *
 270 *
 280 *
 290 *
 300 *
 ACCCCTGGGC TCCACTTACC TGCCCCCTGC TCCTTCAGGG ATGGAGGCAA
 TGGGGACCCG AGGTGAATGG ACGGGGGACG AGGAAGTCCC TACCTCCGTT
 MetGluAla>
 310 *
 320 *
 330 *
 340 *
 350 *
 TGGCGGCCAG CACTTCCCTG CCTGACCCCTG GAGACTTTGA CGGAAACGTG
 ACCGCCGGTC GTGAAGGGAC GGACTGGGAC CTCTGAAACT GGCCTTCGAC
 MetAlaAlaSer ThrSerLeu ProAspPro GlyAspPheAsp ArgAsnVal>
 360 *
 370 *
 380 *
 390 *
 400 *
 CCCCGGATCT GTGGGTGTG TGGAGACCGA GCCACTGGCT TTCACTTCAA
 GGGGCTAGA CACCCACAC ACCTCTGGCT CGGTGACCGA AAGTGAAGTT
 ProArgIle CysGlyValCys GlyAspArg AlaThrGly PheHisPheAsn>
 410 *
 420 *
 430 *
 440 *
 450 *
 TGCTATGACC TGTGAAGGCT GCAAAGGCTT CTTCAAGGCCA AGCATGAAGC
 ACGATACTGG ACACTTCCGA CGTTCCGAA GAAGTCCGCT TCGTACTTCG
 AlaMetThr CysGluGly CysLysGlyPhe PheArgArg SerMetLys>
 460 *
 470 *
 480 *
 490 *
 500 *
 GGAAGGCACT ATTCAACCTGC CCCTCAACG GGGACTGCCG CATCACCAAG
 CCTTCCGTGA TAAGTGGACG GGGAAAGTTGC CCCTGACGGC GTAGTGGTTC
 ArgLysAlaLeu PheThrCys ProPheAsn GlyAspCysArg IleThrLys>

FIG. 8B

510 520 530 540 550
 * * * * *
 GACAACCGAC GCCACTGCCA GGCTGCCGG CTCAAACGCT GTGTGGACAT
 CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTGCGA CACACCTGTA
 AspAsnArg ArgHisCysGln AlaCysArg LeuLysArg CysValAspIle>

 560 570 580 590 600
 * * * * *
 CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC
 GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG
 GlyMetMet LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys>

 610 620 630 640 650
 * * * * *
 GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA GGACAGTCTG
 CCCTCTACTA GGACTTCGCC TTCCTCTCC TCCGGAACCT CCTGTCAGAC
 ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu>

 660 670 680 690 700
 * * * * *
 CGGGCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA
 GCCGGGTTCG ACAGACTCCT CGTCGTCGCC TAGTAACGGT ATGACGACCT
 ArgProLys LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp>

 710 720 730 740 750
 * * * * *
 CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC
 GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG ACGGTCAAGG
 AlaHisHis LysThrTyr AspProThrTyr SerAspPhe CysGlnPhe>

 760 770 780 790 800
 * * * * *
 GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCC
 CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG AAGGTCCGGG
 ArgProProVal ArgValAsn AspGlyGly GlySerHisPro SerArgPro>

 810 820 830 840 850
 * * * * *
 AACTCCAGAC ACACCCCCAG CTTCTCTGGG GACTCCTCCT CCTCCCTGCTC
 TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG
 AsnSerArg HisThrProSer PheSerGly AspSerSer SerSerCysSer>

 860 870 880 890 900
 * * * * *
 AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC AGCTCTCCA
 TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT
 AspHisCys IleThrSer SerAspMetMet AspSerSer SerPheSer>

 910 920 930 940 950
 * * * * *
 ATCTGGATCT GAGTGAAGAA GATTCAAGATG ACCCTCTGT GACCCTAGAG
 TAGACCTAGA CTCACTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC
 AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu>

 960 970 980 990 1000
 * * * * *
 CTGTCCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG
 GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC
 LeuSerGln LeuSerMetLeu ProHisIle AlaAspLeu ValSerTyrSer>

FIG. 8C

1010 * 1020 * 1030 * 1040 * 1050 *
 CATCCAAAAG GTCATTGGCT TTGCTAACAT GATACCAGGA TTCAGAGACC
 GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCT AAGTCTCTGG
 IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp>
 1060 * 1070 * 1080 * 1090 * 1100 *
 TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC
 AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACCTCAG
 LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal>
 1110 * 1120 * 1130 * 1140 * 1150 *
 ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCCCTGGAC
 TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG
 IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr>
 1160 * 1170 * 1180 * 1190 * 1200 *
 CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGT ACCAAAGCCG
 GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC
 CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla>
 1210 * 1220 * 1230 * 1240 * 1250 *
 GACACAGCCT GGAGCTGATT GAGCCCCCTCA TCAAGTTCCA GGTGGGACTG
 CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCCTGAC
 GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu>
 1260 * 1270 * 1280 * 1290 * 1300 *
 AAGAAAGCTGA ACTTGATGA GGAGGAGCAT GTCCTGCTCA TGGCCATCTG
 TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT ACCGGTAGAC
 LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys>
 1310 * 1320 * 1330 * 1340 * 1350 *
 CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG
 GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGCCGC GACTAACTCC
 IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu>
 1360 * 1370 * 1380 * 1390 * 1400 *
 CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC
 GGTAGGTCTT GCGGGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG
 AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg>
 1410 * 1420 * 1430 * 1440 * 1450 *
 CACCCGCCCG CGGGGAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT
 GTGGGCGGGG GCCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA
 HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu>
 1460 * 1470 * 1480 * 1490 * 1500 *
 AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG TACCGCTGCC
 TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC ATGGCGACGG
 AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>

FIG. 8D

1510 1520 1530 1540 1550
* * * * *

TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCT TGTGCTCGAA
AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT
LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>

1560 1570
* *

GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:7)
CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:20)
ValPheGly AsnGluIleSer ***> (SEQ ID NO:12)

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Fig. 1A.

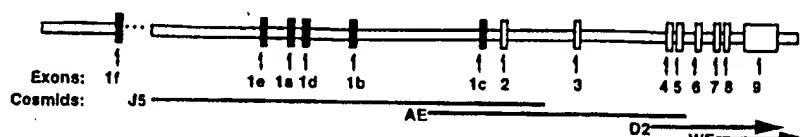


Fig. 1B.

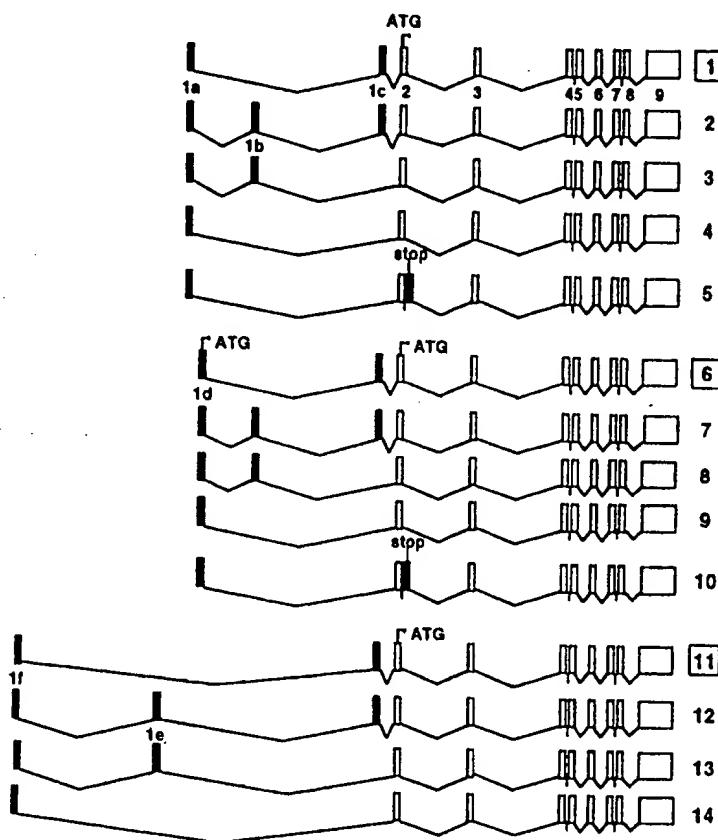


Fig. 1C.

Transcript 1:

MEAMA ASTSL PDPGD FDRNY PRI DBD 427aa

Transcript 6:

MEWRN KKRSD WLSMV LRTAG VEEAF GSEVS VRPHR RAPLG STYLP PAPSG MEAMA ASTSL PDPGD FDRNY PRI DBD 477aa

Transcript 9:

MEW RNKKR SDWLS MVLRT AGVEG MEAMA ASTSL PDPGD FDRNY PRI DBD 450aa

(SEQ ID NO: 14)



(SEQ ID NO: 16)

FIGURE 1

(SEQ ID NO: 15)

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- A. 5'...atcccttaag GGCTCCTGAACCTAGCCCAGCTGGACGGAG
AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCC
CGTGCACATTGCTTGCTTGCTCCCTCAATCCTCATAGCT
TCTCTTGGGgttaagtacag...3' (SEQ ID NO: 13)
- B. 5'...TGCGACCTTGGCGGTGAGCCTGGGACAGGGGTGAGGC
CAGAGACGGACGGACCGCAGGGGCCCGGCCAAGGOGAGGG
AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGCGGTGTG
TTCACCCGCAGCCCAATCCATCACTCAGCAACTCCTAGAC
GCTGGTAGAAAGTTCCCTCCGAGGGAGCCTGCCATCCAGTCGT
GCGTGCAG...3' (SEQ ID NO: 5)
- C. 5'...tgtttttag AGGCAGCATGAAACAGTGGATGTGCAGAG
AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT
AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA
CGGTATTTTACTCTCATGTCTGAAAAGGCTATGATAA
AGATCAAgtaagatatt...3' (SEQ ID NO: 6)
- D. 5'...GTTTCCCTCTCTGTCGGGGCGCCTGGCATGAGTG
GAGGAATAAGAAAAGGAGCGATTGGCTGTCGATGGTCTCA
GAACTGCTGGAGTGGAGGGgtgtaacc...3' (SEQ ID NO: 1)

FIG. 4
FIGURE 4

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FIG. 5A
FIGURE 5A

TRANSCRIPT 6

(Sequence Range: 1 to 1463)

10 20 30 40 50

* * * * *
GTTTCCTTCT TCTGTCGGGG CGCCTTGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
MetGluTrpArg AsnLysLys>

60 70 80 90 100

* * * * *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGAAGC
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCTTCG
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGluAla>

110 120 130 140 150

* * * * *
CTTTGGGTCT GAAGTGTCTG TGAGACCTCA CAGAACAGACA CCCCTGGGCT
GAAACCCAGA CTTCACAGAC ACTCTGGAGT GTCTTCTCGT GGGGACCCGA
PheGlySer GluValSer ValArgProHis ArgArgAla ProLeuGly>

160 170 180 190 200

* * * * *
CCACTTACCT GCCCCCTGCT CCTTCAGGGAA TGGAGGCAAT GGCGGCCAGC
GGTGAATGGA CGGGGACGA GGAAGTCCCT ACCTCCGTTA CCGCCGGTCG
SerThrTyrLeu ProProAla ProSerGly MetGluAlaMet AlaAlaSer>

210 220 230 240 250

* * * * *
ACTTCCCTGC CTGACCCCTGG AGACTTTGAC CGGAACGTGC CCCGGATCTG
TGAAGGGACG GACTGGGACC TCTGAAACTG GCCTTGCACG GGGCCTAGAC
ThrSerLeu ProAspProGly AspPheAsp ArgAsnVal ProArgIleCys>

260 270 280 290 300

* * * * *
TGGGGTGTGT GGAGACCGAG CCACTGGCTT TCACCTCAAT GCTATGACCT
ACCCCACACA CCTCTGGCTC GGTGACCGAA AGTGAAGTTA CGATACTGGA
GlyValCys GlyAspArg AlaThrGlyPhe HisPheAsn AlaMetThr>

310 320 330 340 350

* * * * *
GTGAAGGCTG CAAAGGCTTC TTCAGGGAA GCATGAAGCG GAAGGCACCA
CACTTCCGAC GTTCCGAAG AAGTCCGCTT CGTACTTCGC CTTCCGTGAT
CysGluGlyCys LysGlyPhe PheArgArg SerMetLysArg LysAlaLeu>

360 370 380 390 400

* * * * *
TTCACCTGCC CCTTCAACGG GGACTGCCGC ATCACCAAGG ACAACCGACG
AAGTGGACGG GGAAGTTGCC CCTGACGGCG TAGTGGTTCC TGTGGCTGC
PheThrCys ProPheAsnGly AspCysArg IleThrLys AspAsnArgArg>

FIGURE 5B

-6/20-

410 420 430 440 450
* * * * * * * *
CCACTGCCAG GCCTGCCGGC TCAAAACGCTG TGTGGACATC GGCATGATGA
GGTGACGGTC CGGACGGCCG AGTTTGCAC ACACCTGTAG CCGTACTACT
HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet>

460 470 480 490 500
* * * * * * * *
AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC
TCCTCAAGTA AGACTGTCTA CTCCTTCACG TCTCCTTCGC CCTCTACTAG
LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle>

510 520 530 540 550
* * * * * * * *
CTGAAGCGGA AGGAGGGAGGA GGCCTTGAAG GACAGTCTGC GGCCCAGCT
GACTTCGCCT TCCTCCTCCCT CGGAACTTC CTGTCAGACG CCGGGTTCGA
LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu>

560 570 580 590 600
* * * * * * * *
GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACCATA
CAGACTCCTC GTCGTGCGGT AGAACGGTA TGACGACCTG CGGGTGGTAT
SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis>

610 620 630 640 650
* * * * * * * *
AGACCTACGA CCCCCACCTAC TCCGACTTCT GCCAGTTCCG GCCTCCAGTT
TCTGGATGCT GGGGTGGATG AGGCTGAAGA CGGTCAAGGC CGGAGGTCAA
LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal>

660 670 680 690 700
* * * * * * * *
CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCA ACTCCAGACA
GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT
ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis>

710 720 730 740 750
* * * * * * * *
CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCTGCTCA GATCACTGTA
GTGAGGGTCG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT
ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys>

760 770 780 790 800
* * * * * * * *
TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG
AGTGGAGAAG TCTGTACTAC CTGAGCAGGT CGAACAGGTT AGACCTAGAC
IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu>

810 820 830 840 850
* * * * * * * *
AGTGAAGAAG ATTCAAGATGA CCCTCTGTG ACCCTAGAGC TGTCCCAGCT
TCACCTCTTC TAAGTCTACT GGGAAAGACAC TGGGATCTCG ACAGGGTCGA
SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>

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FIG. 7A

TRANSCRIPT 10

(Sequence Range: 1 to 1534)

10 20 30 40 50
* * * * *
GTTTCCTTCT TCTGTGGGG CGCCTTGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
MetGluTrpArg AsnLysLys>
60 70 80 90 100
* * * * *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>
110 120 130 140 150
* * * * *
GGAGGCAATG GCGGCCACCA CTTCCCTGCC TGACCCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>
160 170 180 190 200
* * * * *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>
210 220 230 240 250
* * * * *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGTGAGC
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCACTCG
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArg***
260 270 280 290 300
* * * * *
CCCCCTCCCA GGCTCTCCCC AGTGGAAAGG GAGGGAGAAG AAGCAAGGTG
GGGGGAGGT CCGAGAGGGG TCACCTTCC CTCCCTCTTC TTCGTTCCAC
310 320 330 340 350
* * * * *
TTTCCATGAA GGGAGCCCTT GCATTTTCA CATCTCCTTC CTTACAATGT
AAAGGTACTT CCCTCGGGAA CGTAAAAAGT GTAGAGGAAG GAATGTTACA
360 370 380 390 400
* * * * *
CCATGGAACA TGCGGCCCTC ACAGCCACAG GAGCAGGAGG GTCTTGGCGA
GGTACCTTGT ACGCCGCGAG TGTCGGTGTG CTCGTCCTCC CAGAACCGCT



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FIG. 7B
-14720-

410 420 430 440 450
* * * * * *
AGCATGAAGC GGAAGGCAC ATTACACCTGC CCCTTCAACG GGGACTGCCG
TCGTACTTCG CCTTCCGTGA TAAGTGGACG GGGAAAGTTGC CCCTGACGGC

460 470 480 490 500
* * * * * *
CATCACCAAG GACAACCGAC GCCACTGCCA GGCCCTGCCGG CTCAAACGCT
GTAGTGGTTC CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCAG

510 520 530 540 550
* * * * * *
GTGTGGACAT CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG
CACACCTGTA GCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC

560 570 580 590 600
* * * * * *
CAGAGGAAGC GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA
GTCTCCTTCG CCCTCTACTA GGACTTCGCC TTCCCTCCTCC TCCGGAACCT

610 620 630 640 650
* * * * * *
GGACAGTCTG CGGCCAACAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA
CCTGTCAGAC GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT

660 670 680 690 700
* * * * * *
TACTGCTGGA CGCCCCACCAT AAGACCTACG ACCCCCACCTA CTCCGACTTC
ATGACGACCT GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG

710 720 730 740 750
* * * * * *
TGCCAGTTCC GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC
ACGGTCAAGG CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG

760 770 780 790 800
* * * * * *
TTCCAGGCC AACTCCAGAC ACACCTCCAG CTCTCTGGG GACTCCTCCT
AAGGTCCGGG TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA

810 820 830 840 850
* * * * * *
CCTCCTGTC AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC
GGAGGACGAG TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG

860 870 880 890 900
* * * * * *
AGCTCTCCA ATCTGGATCT GAGTGAAGAA GATTCAAGATG ACCCTTCTGT
TCGAAGAGGT TAGACCTAGA CTCACCTCTT CTAAGTCTAC TGGGAAGACA

910 920 930 940 950
* * * * * *
GACCCTAGAG CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG
CTGGGATCTC GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC

FIG. 7C
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960 970 980 990 1000
TCAGTTACAG CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA
AGTCAATGTC GTAGGTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT
1010 1020 1030 1040 1050
TTCAGAGACC TCACCTCTGA GGACAGATC GTACTGCTGA AGTCAAGTGC
AAGTCTCTGG AGTGGAGACT CCTGGTCTAG CATGAGGACT TCAGTTCACG
1060 1070 1080 1090 1100
CATGGAGTC ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA
GTAACCTCCAG TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT
1110 1120 1130 1140 1150
TGTCCTGGAC CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG
ACAGGACCTG GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC
1160 1170 1180 1190 1200
ACCAAAGCCG GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA
TGGTTTCGGC CTGTGTCGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT
1210 1220 1230 1240 1250
GGTGGGACTG AAGAAGCTGA ACTTGATGA GGAGGAGCAT GTCCTGCTCA
CCACCCCTGAC TTCTTCGACT TGAACGTA CTCCTCGTA CAGGACGAGT
1260 1270 1280 1290 1300
TGGCCATCTG CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG
ACCGGTAGAC GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC
1310 1320 1330 1340 1350
CTGATTGAGG CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT
GACTAACTCC GGTAGGTCTT GGCGGACAGG TTGTGTGAGC TCTGCATGTA
1360 1370 1380 1390 1400
CCGCTGCCGC CACCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA
GGCGACGGCG GTGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT
1410 1420 1430 1440 1450
TCCAGAAAGCT AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG
AGGTCTCGA TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC
1460 1470 1480 1490 1500
TACCGCTGCC TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCT
ATGGCGACGG AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA

Title: "Isoforms of the Human Vitamin D Receptor"
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Atty. Docket No. RICE-014

PCT/AU98/00817



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FIG. 7D
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1510 1520 1530

* * *

TGTGCTCGAA GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:4)
ACACGAGCTT CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:19)

FIG. 8A

FIGURE 8

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10 20 30 40 50
* * * * *
TGCGACCTTG GCGGTGAGCC TGGGGACAGG GGTGAGGCCA GAGACGGACG
ACGCTGGAAC CGCCACTCGG ACCCCTGTCC CCACTCCGGT CTCTGCCTGC
60 70 80 90 100
* * * * *
GACGCAGGGG CCCGGGCCAA GGCAGGGAG AACAGCGCA CTAAGGCAGA
CTGCGTCCC GGGCCGGGTT CCGCTCCCTC TTGTGCCGT GATTCCGTCT
110 120 130 140 150
* * * * *
AAGGAAGAGG GCGGTGTTT CACCCGCAGC CCAATCCATC ACTCAGCAAC
TTCCTTCTCC CGCCACACAA GTGGGCGTCG GGTTAGGTAG TGAGTCGTTG
160 170 180 190 200
* * * * *
TCCTAGACGC TGGTAGAAAG TTCCTCCAG GAGCCTGCCA TCCAGTCGTG
AGGATCTGCG ACCATCTTC AAGGAGGCTC CTCGGACGGT AGGTCAAGCAC
210 220 230 240 250
* * * * *
CGTGCAGAAG CCTTTGGGTC TGAAGTGTCT GTGAGACCTC ACAGAAGAGC
GCACGTCTTC GGAAACCCAG ACTTCACAGA CACTCTGGAG TGTCTTCTCG
260 270 280 290 300
* * * * *
ACCCCTGGGC TCCACTTACC TGCCCCCTGC TCCTTCAGGG ATGGAGGCAA
TGGGGACCCG AGGTGAATGG ACGGGGGACG AGGAAGTCCC TACCTCCGTT
MetGluAla>
310 320 330 340 350
* * * * *
TGGCGGCCAG CACTTCCCTG CCTGACCTG GAGACTTGA CCGGAACGTG
ACCGCCGGTC GTGAAGGGAC GGACTGGGAC CTCTGAAACT GGCCTTGCAC
MetAlaAlaSer ThrSerLeu ProAspPro GlyAspPheAsp ArgAsnVal>
360 370 380 390 400
* * * * *
CCCCGGATCT GTGGGGTGTG TGGAGACCGA GCCACTGGCT TTCACTTCAA
GGGGCCTAGA CACCCACAC ACCTCTGGCT CGGTGACCGA AAATGAAGTT
ProArgIle CysGlyValCys GlyAspArg AlaThrGly PheHisPheAsn>
410 420 430 440 450
* * * * *
TGCTATGACC TGTGAAGGCT GCAAAGGCTT CTTCAAGCGA AGCATGAAGC
ACGATACTGG ACACCTCCGA CGTTCCGAA GAAGTCCGCT TCGTACTTCG
AlaMetThr CysGluGly CysLysGlyPhe PheArgArg SerMetLys>
460 470 480 490 500
* * * * *
GGAAGGCAC ATTACACCTGC CCCTCAACG GGGACTGCCG CATCACCAAG
CCTTCCGTGA TAAGTGGACG GGGAAAGTTGC CCCTGACGGC GTAGTGGITC
ArgLysAlaLeu PheThrCys ProPheAsn GlyAspCysArg IleThrLys>

FIG. 8B
18/20

510 520 530 540 550
* * * * *
GACAACCGAC GCCACTGCCA GGCTGCCGG CTCAAACGCT GTGTGGACAT
CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCAG CACACCTGTA
AspAsnArg ArgHisCysGln AlaCysArg LeuLysArg CysValAspIle>

560 570 580 590 600
* * * * *
CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC
GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG
GlyMetMet LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys>

610 620 630 640 650
* * * * *
GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTGAA GGACAGTCTG
CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACCT CCTGTCAGAC
ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu>

660 670 680 690 700
* * * * *
CGGCCAACGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA
GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGAACGGT ATGACGACCT
ArgProLys LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp>

710 720 730 740 750
* * * * *
CGCCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC
GCAGGGTGGTA TTCTGGATGC TGAGGTGGAT GAGGCTGAAG ACGGTCAAGG
AlaHisHis LysThrTyr AspProThrTyr SerAspPhe CysGlnPhe>

760 770 780 790 800
* * * * *
GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCC
CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG AAGGTCCGGG
ArgProProVal ArgValAsn AspGlyGly GlySerHisPro SerArgPro>

810 820 830 840 850
* * * * *
AACTCCAGAC ACACCTCCAG CTTCTCTGGG GACTCCTCCT CCTCCTGCTC
TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG
AsnSerArg HisThrProSer PheSerGly AspSerSer SerSerCysSer>

860 870 880 890 900
* * * * *
AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC AGCTTCTCCA
TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT
AspHisCys IleThrSer SerAspMetMet AspSerSer SerPheSer>

910 920 930 940 950
* * * * *
ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTCTGT GACCCTAGAG
TAGACCTAGA CTCACCTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC
AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu>

960 970 980 990 1000
* * * * *
CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG
GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC
LeuSerGln LeuSerMetLeu ProHisLeu AlaAspLeu ValSerTyrSer>

O I P E
OCT 22 2002
WO-99/16872

Title: "Isoforms of the Human Vitamin D Receptor"
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Atty. Docket No. RICE-014

PCT/AU98/00817

FIG. 8C

19720

1010 1020 1030 1040 1050
* * * * *
CATCCAAAAG GTCATGGCT TTGCTAAGAT GATACCAGGA TTCAGAGACC
GTAGGTTTC CACTAACCGA AACGATTCTA CTATGGCTCT AAGTCTCTGG
IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp>
1060 1070 1080 1090 1100
* * * * *
TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC
AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACCTCCAG
LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal>
1110 1120 1130 1140 1150
* * * * *
ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCCCTGGAC
TAGTACAAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG
IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr>
1160 1170 1180 1190 1200
* * * * *
CTGTTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG
GACACCCTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC
CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla>
1210 1220 1230 1240 1250
* * * * *
GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA GGTGGGACTG
CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCCTGAC
GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu>
1260 1270 1280 1290 1300
* * * * *
AAGAAAGCTGA ACTTGCATGA GGAGGGAGCAT GTCCTGCTCA TGGCCATCTG
TTCTTCGACT TGAACGACT CTCCTCGTA CAGGACGAGT ACCGGTAGAC
LysLysLeu AshLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys>
1310 1320 1330 1340 1350
* * * * *
CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG
GTAGCAGAGG GGTCTAGCAG GACCCACGT CCTGGGGCGC GACTAACTCC
IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu>
1360 1370 1380 1390 1400
* * * * *
CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC
GGTAGGTCTT GGCAGGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG
AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg>
1410 1420 1430 1440 1450
* * * * *
CACCCGCCCG CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAACGCT
GTGGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA
HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu>
1460 1470 1480 1490 1500
* * * * *
AGCCGACCTG CGCAGCCCTCA ATGAGGGAGCA CTCCAAGCAG TACCGCTGCC
TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC ATGGCGACGG
AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>

O I P E
OCT 22 2002
WO 99/16872
PATENT & TRADEMARK OFFICE
Title: "Isoforms of the Human Vitamin D Receptor"
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Atty. Docket No. RICE-014

PCT/AU98/00817

FIG. 8D
20/20

1510 1520 1530 1540 1550
* * * * *

TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCT TGTGCTCGAA
AGAGGAAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT
LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>

1560 1570

* *

GTGTTGGCA ATGAGATCTC CTGA (SEQ ID NO: 7)
CACAAACCGT TACTCTAGAG GACT (SEQ ID NO: 20)
ValPheGly AsnGluIleSer ***>(SEQ ID NO: 12)

FIG. 5C

770
860 870 880 890 900
CTCCATGCTG CCCCACCTGG CTGACCTGGT CAGTTACAGC ATCCAAAAGG
GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG TAGGTTTCC
SerMetLeu ProHisLeu AlaAspLeuVal SerTyrSer IleGlnLys>
910 920 930 940 950
TCATTGGCTT TGCTAAAGATG ATACCAGGAT TCAGAGACCT CACCTCTGAG
AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA GTGGAGACTC
ValIleGlyPhe AlaLysMet IleProGly PheArgAspLeu ThrSerGlu>
960 970 980 990 1000
GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTCA TCATGTTGCC
CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAGT AGTACAACGC
AspGlnIle ValLeuLeuLys SerSerAla IleGluVal IleMetLeuArg>
1010 1020 1030 1040 1050
CTCCAATGAG TCCTTCACCA TGGACGACAT GTCTGGACC TGTGGCAACC
GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCTGG ACACCGTTGG
SerAsnGlu SerPheThr MetAspAspMet SerTrpThr CysGlyAsn>
1060 1070 1080 1090 1100
AAGACTACAA GTACCGCGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG
TTCTGATGTT CATGGCGCAG TCACTGCACT GGTTTCGGCC TGTGTCGGAC
GlnAspTyrLys TyrArgVal SerAspVal ThrLysAlaGly HisSerLeu>
1110 1120 1130 1140 1150
GAGCTGATTG AGCCCCTCAT CAAGTTCCAG GTGGGACTGAA AGAACGCTGAA
CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCCCTGACT TCTTCGACTT
GluLeuIle GluProLeuIle LysPheGln ValGlyLeu LysLysLeuAsn>
1160 1170 1180 1190 1200
CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC
GAACGTACTC CTCCTCGTAC AGGACGAGTA CCGGTAGAGC TAGCAGAGGG
LeuHisGlu GluGluHis ValLeuLeuMet AlaIleCys IleValSer>
1210 1220 1230 1240 1250
CAGATCGTC CGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC
GTCTAGCAGG ACCCACGTC CTGCGGCGCG ACTAACTCCG GTAGGTCTG
ProAspArgPro GlyValGln AspAlaAla LeuIleGluAla IleGlnAsp>
1260 1270 1280 1290 1300
CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCC
GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGGGGGGG
ArgLeuSer AsnThrLeuGln ThrTyrIle ArgCysArg HisProProPro>

FIG. 5D

8/20

1310 1320 1330 1340 1350

* * * * * * * * * *

GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC
CCCGTCGGTG GACGAGATAC GGTTCTACTA GGTCTTCGAT CGGCTGGACG
GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu>

1360 1370 1380 1390 1400

* * * * * * * * * *

GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG
CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGCGACGGA GAGGAAGGTC
ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln>

1410 1420 1430 1440 1450

* * * * * * * * * *

CCTGAGTGCA GCATGAAGCT AACGCCCTT GTGCTCGAAG TGTTTGGCAA
GGACTCACGT CGTACTTCGA TTGCGGGAA CACGAGCTTC ACAAACCGTT
ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn>

1460

* *
TGAGATCTCC TGA (SEQ ID NO: 2)
ACTCTAGAGG ACT (SEQ ID NO: 17)
GluIleSer ***> (SEQ ID NO: 9)

9/20

FIG. 6A

FIGURE 6

TRANSCRIPT 9

(Sequence Range: 1 to 1382)

10 20 30 40 50
* * * * *
GTTTCCCTTCT TCTGTGGGG CGCCTTGGCA TGAGATGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
MetGluTrpArg AsnLysLys>

60 70 80 90 100
* * * * *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

110 120 130 140 150
* * * * *
GGAGGCAATG GCGGCCAGCA CTTCCTGCG TGACCCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

160 170 180 190 200
* * * * *
GGAACGTGCC CGGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GCCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

210 220 230 240 250
* * * * *
CACTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGCCAAG
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTCCGAAGA AGTCCGCTTC
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArgArgSer>

260 270 280 290 300
* * * * *
CATGAAGCGG AAGGCACTAT TCACCTGCC CTTAACGGG GACTGCCGCA
GTACTTCGCC TTCCGTGATA AGTGGACGGG GAAGTTGCCCTTGACGGCGT
MetLysArg LysAlaLeu PheThrCysPro PheAsnGly AspCysArg>

310 320 330 340 350
* * * * *
TCACCAAGGA CAACCGACGC CACTGCCAGG CCTGCCGGCT CAAACGCTGT
AGTGGTTCCT GTTGGCTGCG GTGACGGTCC GGACGGCCGA GTTTGCGACA
IleThrLysAsp AsnArgArg HisCysGln AlaCysArgLeu LysArgCys>

360 370 380 390 400
* * * * *
GTGGACATCG GCATGATGAA GGAGTCATT CTGACAGATG AGGAAGTGCA
CACCTGTAGC CGTACTACTT CCTCAAGTAA GACTGTCTAC TCCTTCACGT
ValAspIle GlyMetMetLys GluPheIle LeuThrAsp GluGluValGln>

FIG. 6B
10/20

410 420 430 440 450

* * * * *
GAGGAAGCGG GAGATGATCC TGAAGCGGAA GGAGGGAGGAG GCCTTGAAGG
CTCCTTCGCC CTCTACTAGG ACTTCGCCTT CCTCCTCCTC CGGAACCTCC
ArgLysArg GluMetIle LeuLysArgLys GluGluGlu AlaLeuLys>

460 470 480 490 500

* * * * *
ACAGTCTGCG GCCCAAGCTG TCTGAGGAGC AGCAGCGCAT CATTGCCATA
TGTCAAGACGC CGGGTTCGAC AGACTCCTCG TGTCGCGTA GTAACGGTAT
AspSerLeuArg ProLysLeu SerGluGlu GlnGlnArgIle IleAlaIle>

510 520 530 540 550

* * * * *
CTGCTGGACG CCCACCATAA GACCTACGAC CCCACCTACT CCGACTTCTG
GACGACCTGC GGGTGGTATT CTGGATGCTG GGGTGGATGA GGCTGAAGAC
LeuLeuAsp AlaHisHisLys ThrTyrAsp ProThrTyr SerAspPheCys>

560 570 580 590 600

* * * * *
CCAGTTCCGG CCTCCAGTTC GTGTGAATGA TGGTGGAGGG AGCCATCCTT
GGTCAAGGCC GGAGGTCAAGCACACTACT ACCACCTCCC TCGGTAGGAA
GlnPheArg ProProVal ArgValAsnAsp GlyGlyGly SerHisPro>

610 620 630 640 650

* * * * *
CCAGGGCCAA CTCCAGACAC ACTCCCAGCT TCTCTGGGA CTCCTCCTCC
GGTCCGGGTT GAGGTCTGTG TGAGGGTCGA AGAGACCCCT GAGGAGGAGG
SerArgProAsn SerArgHis ThrProSer PheSerGlyAsp SerSerSer>

660 670 680 690 700

* * * * *
TCCTGCTCAG ATCACTGTAT CACCTCTCA GACATGATGG ACTCGTCCAG
AGGACGAGTC TAGTGACATA GTGGAGAAAGT CTGTACTACC TGAGCAGGTC
SerCysSer AspHisCysIle ThrSerSer AspMetMet AspSerSerSer>

710 720 730 740 750

* * * * *
CTTCTCCAAT CTGGATCTGA GTGAAGAAGA TTCAGATGAC CCTTCTGTGA
GAAGAGGTAA GACCTAGACT CACTCTTCT AAGTCTACTG GGAAGACACT
PheSerAsn LeuAspLeu SerGluGluAsp SerAspAsp ProSerVal>

760 770 780 790 800

* * * * *
CCCTAGAGCT GTCCCAGCTC TCCATGCTGC CCCACCTGGC TGACCTGGTC
GGGATCTCGA CAGGGTCGAG AGGTACGACG GGGTGGACCG ACTGGACCAG
ThrLeuGluLeu SerGlnLeu SerMetLeu ProHisLeuAla AspLeuVal>

810 820 830 840 850

* * * * *
AGTTACAGCA TCCAAAAGGT CATTGGCTTT GCTAAGATGA TACCAGGATT
TCAATGTCGT AGGTTTCCA GTAACCGAAA CGATTCTACT ATGGTCCTAA
SerTyrSer IleGlnLysVal IleGlyPhe AlaLysMet IleProGlyPhe>

FIG. 6C
11/20

860 870 880 890 900
* * * * * *
CAGAGACCTC ACCTCTGAGG ACCAGATCGT ACTGCTGAAG TCAAGTGCCA
GTCTCTGGAG TGGAGACTCC TGGTCTAGCA TGACGACTTC AGTTCACGGT
ArgAspLeu ThrSerGlu AspGlnIleVal LeuLeuLys SerSerAla>

910 920 930 940 950
* * * * * *
TTGAGGTCAT CATGTTGCGC TCCAATGAGT CCTTCACCAC GGACGACATG
AACTCCAGTA GTACAACGCG AGGTTACTCA GGAAGTGGTA CCTGCTGTAC
IleGluValIle MetLeuArg SerAsnGlu SerPheThrMet AspAspMet>

960 970 980 990 1000
* * * * * *
TCCTGGACCT GTGGCAACCA AGACTACAAG TACCGCGTCA GTGACGTGAC
AGGACCTGGA CACCGTTGGT TCTGATGTT ATGGCGCAGT CACTGCACTG
SerTrpThr CysGlyAsnGln AspTyrLys TyrArgVal SerAspValThr>

1010 1020 1030 1040 1050
* * * * * *
CAAAGCCGGA CACAGCCTGG AGCTGATTGA GCCCCTCATC AAGTTCCAGG
GTTTCGGCCT GTGTCGGACC TCGACTAACT CGGGGAGTAG TTCAAGGTCC
LysAlaGly HisSerLeu GluLeuIleGlu ProLeuIle LysPheGln>

1060 1070 1080 1090 1100
* * * * * *
TGGGACTGAA GAAGCTGAAC TTGCATGAGG AGGAGCATGT CCTGCTCATG
ACCCCTGACTT CTTCGACTTG AACGTACTCC TCCTCGTACA GGACGAGTAC
ValGlyLeuLys LysLeuAsn LeuHisGlu GluGluHisVal LeuLeuMet>

1110 1120 1130 1140 1150
* * * * * *
GCCATCTGCA TCGTCTCCCC AGATCGTCCT GGGGTGCAGG ACGCCGCGCT
CGGTAGACGT AGCAGAGGGG TCTAGCAGGA CCCCACGTCC TGCAGCGCGA
AlaIleCys IleValSerPro AspArgPro GlyValGln AspAlaAlaLeu>

1160 1170 1180 1190 1200
* * * * * *
GATTGAGGCC ATCCAGGACC GCCTGTCCAA CACACTGCAG ACGTACATCC
CTAACTCCGG TAGGTCTGG CGGACAGGTT GTGTGACGTC TGCATGTAGG
IleGluAla IleGlnAsp ArgLeuSerAsn ThrLeuGln ThrTyrIle>

1210 1220 1230 1240 1250
* * * * * *
GCTGCCGCCA CCCGCCCCCG GGCAGCCACC TGCTCTATGC CAAGATGATC
CGACGGCGGT GGGCGGGGGC CCGTCGGTGG ACCAGATACG GTTCTACTAG
ArgCysArgHis ProProPro GlySerHis LeuLeuTyrAla LysMetIle>

1260 1270 1280 1290 1300
* * * * * *
CAGAACGCTAG CCGACCTGCG CAGCCTCAAT GAGGAGCACT CCAAGCAGTA
GTCTCGATC GGCTGGACGC GTCGGAGTTA CTCCCTCGTGA GGTTCGTCAT
GlnLysLeu AlaAspLeuArg SerLeuAsn GluGluHis SerLysGlnTyr>

WO 99/16872

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FIG. 6D
12/20

1310 1320 1330 1340 1350

* * * * *

CCGCTGCCTC TCCTTCCAGC CTGAGTCAG CATGAAGCTA ACGCCCCTG
GGCGACGGAG AGGAAGGTG GACTCACGTC GTACTTCGAT TGCGGGGAAC
ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>

1360 1370 1380

* * * * *

TGCTCGAACGT GTTTGGCAAT GAGATCTCCT GA (SEQ ID NO: 3)
ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT (SEQ ID NO: 18)
ValLeuGluVal PheGlyAsn GluIleSer ***>(SEQ ID NO: 10)